



Box Sequence

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: DIXIT, VISHVA M.
- (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING FAS-ASSOCIATED APOPTOSIS
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Morrison & Foerster
 - (B) STREET: 755 Page Mill Road
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/443,982
 - (B) FILING DATE: 18-MAY-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Konski, Antoinette F.
 - (B) REGISTRATION NUMBER: 34,202
 - (C) REFERENCE/DOCKET NUMBER: 20344-21070.20
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (415)813-5600
 - (B) TELEFAX: (415)494-0792
 - (C) TELEX: 706141 MRSNFOERS SFO

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1642 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 130..756
- (ix) FEATURE:
- (A) NAME/KEY: misc_feature
 - (B) LOCATION: 4..6
 - (D) OTHER INFORMATION: /note= "An in-frame stop codon 130 base pairs upstream of the initiator methionine"
- (ix) FEATURE:
- (A) NAME/KEY: polyA_signal
 - (B) LOCATION: 1636..1641
 - (D) OTHER INFORMATION: /note= "Potential poly(A) adenylation signal"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 198..753
 (D) OTHER INFORMATION: /note= "Clone-15, 5' end of FADD"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 249..753
 (D) OTHER INFORMATION: /note= "Clone-8, 5' end of FADD"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 177..658
 (D) OTHER INFORMATION: /note= "Death Domain of FADD"

(ix) FEATURE:
 (A) NAME/KEY: mutation
 (B) LOCATION: replace(490..492, "")
 (D) OTHER INFORMATION: /note= "For FADDmt, the sequence is altered to either AAT or AAC and the corresponding codon from Val to Asn"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: group(250..753, 232..753)
 (D) OTHER INFORMATION: /note= "Corresponding amino acids can comprise C-terminal polypeptide fragments of FADD"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 253..753
 (D) OTHER INFORMATION: /note= "Corresponding amino acids can comprise a polypeptide fragment of FADD designated NFD-2"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 310..753
 (D) OTHER INFORMATION: /note= "Corresponding amino acids can comprise a polypeptide fragment of FADD designated NFD-3"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 367..753
 (D) OTHER INFORMATION: /note= "Corresponding amino acids can comprise polypeptide fragment of FADD designated NFD-4"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 131..504
 (D) OTHER INFORMATION: /note= "Corresponding amino acids can comprise an N-terminal half polypeptide fragment of FADD"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 71..478
 (D) OTHER INFORMATION: /note= "Corresponding amino acids can comprise an N-terminal half polypeptide fragment of FADD designated N-FADD"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 133..501
 (D) OTHER INFORMATION: /note= "Corresponding amino acids can comprise an N-terminal half polypeptide fragment of FADD"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG	60
GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA	120
GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCG TCC	168
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser	
1 5 10	
AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG	216
Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly	
15 20 25	
CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC	264
Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu	
30 35 40 45	
TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG	312
Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu	
50 55 60	
CTC CTG CGC GAG CTG CTC GCC TCC CTG CGG CGC CAC GAC CTG CTG CGG	360
Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg	
65 70 75	
CGC GTC GAC GAC TTC GAG GCG GGG GCG GCG GCC GGG GCC GCG CCT GGG	408
Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly	
80 85 90	
GAA GAA GAC CTG TGT GCA GCA TTT AAC GTC ATA TGT GAT AAT GTG GGG	456
Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly	
95 100 105	
AAA GAT TGG AGA AGG CTG GCT CGT CAG CTC AAA GTC TCA GAC ACC AAG	504
Lys Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys	
110 115 120 125	
ATC GAC AGC ATC GAG GAC AGA TAC CCC CGC AAC CTG ACA GAG CGT GTG	552
Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val	
130 135 140	
CGG GAG TCA CTG AGA ATC TGG AAG AAC ACA GAG AAG GAG AAC GCA ACA	600
Arg Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr	
145 150 155	
GTG GCC CAC CTG GTG GGG GCT CTC AGG TCC TGC CAG ATG AAC CTG GTG	648
Val Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val	
160 165 170	
GCT GAC CTG GTA CAA GAG GTT CAG CAG GCC CGT GAC CTC CAG AAC AGG	696
Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg	
175 180 185	
AGT GGG GCC ATG TCC CCG ATG TCA TGG AAC TCA GAC GCA TCT ACC TCC	744
Ser Gly Ala Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser	
190 195 200 205	
GAA GCG TCC TGA TGGGCCGCTG CTTTGCCTG GTGGACCACA GGCATCTACA	796
Glu Ala Ser *	
CAGCCTGGAC TTTGGTTCTC TCCAGGAAGG TAGCCCAGCA CTGTGAAGAC CCAGCAGGAA	856
GCCAGGCTGA GTGAGCCACA GACCACCTGC TTCTGAACTC AAGCTGCGTT TATTAATGCC	916

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cont

TCTCCCGCAC CAGGCCGGGC TTGGGCCCTG CACAGATATT TCCATTTCTT CCTCACTATG 976
 ACACTGAGCA AGATCTTGTC TCCACTAAAT GAGCTCCTGC GGGAGTAGTT GGAAAGTTGG 1036
 AACCGTGTCC AGCACAGAAG GAATCTGTGC AGATGAGCAG TCACACTGTT ACTCCACAGC 1096
 GGAGGAGACC AGCTCAGAGG CCCAGGAATC GGAGCGAAGC AGAGAGGTGG AGAACTGGGA 1156
 TTTGAACCCC CGCCATCCTT CACCAGAGCC CATGCTCAAC CACTGTGGCG TTCTGCTGCC 1216
 CCTGCAGTTG GCAGAAAGGA TGTTTTGTCC CATTTCCTTG GAGGCCACCG GGACAGACCT 1276
 GGACACTAGG GTCAGGCGGG GTGCTGTGGT GGGGAGAGGC ATGGCTGGGG TGGGGGTGGG 1336
 GAGACCTGGT TGGCCGTGGT CCAGCTCTTG GCCCCTGTGT GAGTTGAGTC TCCTCTCTGA 1396
 GACTGCTAAG TAGGGGCAGT GATGGTTGCC AGGACGAATT GAGATAATAT CTGTGAGGTG 1456
 CTGATGAGTG ATTGACACAC AGCACTCTCT AAATCTTCCT TGTGAGGATT ATGGGTCCTG 1516
 CAATTCTACA GTTTCTTACT GTTTTGTATC AAAATCACTA TCTTTCTGAT AACAGAATTG 1576
 CCAAGGCAGC GGGATCTCGT ATCTTTAAAA AGCAGTCCTC TTATTCCTAA GGTAATCCTA 1636
 TTAAAA 1642

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
 1 5 10 15
 Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly
 20 25 30
 Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
 35 40 45
 Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
 50 55 60
 Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
 65 70 75 80
 Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
 85 90 95
 Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
 100 105 110
 Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
 115 120 125
 Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
 130 135 140

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 Cont.

Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
145 150 155 160
Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
165 170 175
Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
180 185 190
Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
195 200 205

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "V is replaced by asparagine(N) for the point mutant of hFADD"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile
1 5 10 15
Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg
20 25 30
Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val
35 40 45
Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala
50 55 60
Asp Leu Val Gln Glu Val
65 70

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "I is replaced by asparagine(N) for the point mutant of rFas"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Ala Lys Lys Phe Ala Arg Gln His Lys Ile Pro Glu Ser Lys Ile
1 5 10 15
Asp Glu Ile Glu His Asn Ser Pro Gln Asp Ala Ala Glu Gln Lys Ile
20 25 30
Gln Leu Leu Gln Cys Trp Tyr Gln Ser His Gly Lys Thr Gly Ala Cys
35 40 45
Gln Ala Leu Ile Gln Gly Leu Arg Lys Ala Asn Arg Cys Asp Ile Ala
50 55 60
Glu Glu Ile Gln Ala Met
65 70

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "V is replaced by asparagine(N) for the point mutant of hFas"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile
1 5 10 15
Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val
20 25 30
Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr
35 40 45
Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala
50 55 60
Glu Lys Ile Gln Thr Ile
65 70

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11

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Cont.

(D) OTHER INFORMATION: /note= "L is replaced by asparagine for the point mutant of hTNFR-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu Ile
1 5 10 15
Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr
20 25 30
Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr
35 40 45
Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys
50 55 60
Leu Glu Asp Ile Glu Glu
65 70

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCCTGGTA CCATGCTGGG CATCTGGACC CTCCTACCTC TGGTTCTTAC GTCTGTTGCT 60
AGATTATCGT CCAAAGACTA CAAGGACGAC GATGACAAGA GTGTTAATGC CCAAGTC 117

a4
cont.